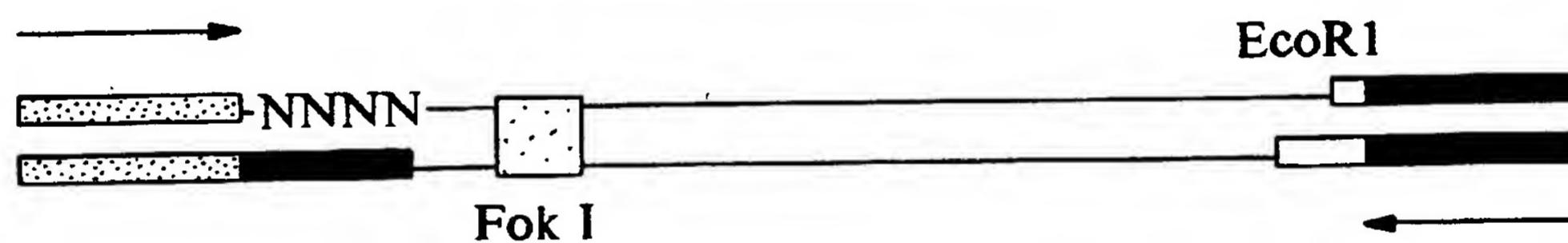
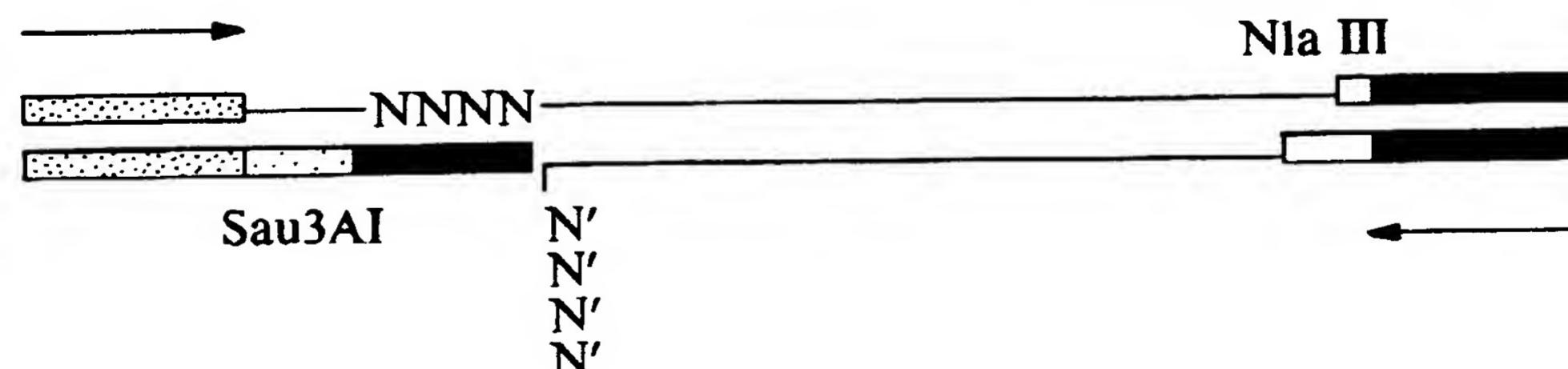


I. Primer-directed (AFLP)**II. Adapter-directed****Class IIIS****Class II****FIG. 1**

Sau3AI

The diagram illustrates the synthesis of a displacement structure from a restriction fragment and an adaptor.

Restriction Fragment: A single-stranded DNA sequence starting with **Y-X** and ending with **C-T-A-G**. The 5' end is at the top, indicated by a vertical bar with a horizontal dash. The 3' end is at the bottom, indicated by a vertical bar with a wavy line.

Adaptor: A synthetic DNA sequence consisting of an **Indexing Sequence** (labeled X) followed by a sequence of **G-A-T-C**.

Displacement Structure: The final product is a double-stranded molecule. The top strand is labeled **xxxx 3'** and the bottom strand is labeled **5'**. The strands are composed of the following base pairs:

- Top strand (5' end): T-A, G-C, A-T, C-G, C-G, G-C, G-C, C-G, A-T, G-C, C-G, A-T, A-T, A-T, T-A, G-C, T-A.
- Bottom strand (3' end): Y-X, Y-X, Y-X, Y-X, C-G, T-A, A-T, G-C, C-G, C-G, G-C, G-C, C-G, A-T, G-C, C-G, A-T, A-T, A-T, T-A, G-C, T-A.

A curved arrow labeled **ligation** points to the junction where the adaptor sequence is joined to the restriction fragment. A small triangle (Δ) is located near the bottom right of the displaced strand.

Strand Labels:

- primer strand:** Points to the bottom strand.
- invading strand:** Points to the top strand.

FIG. 2

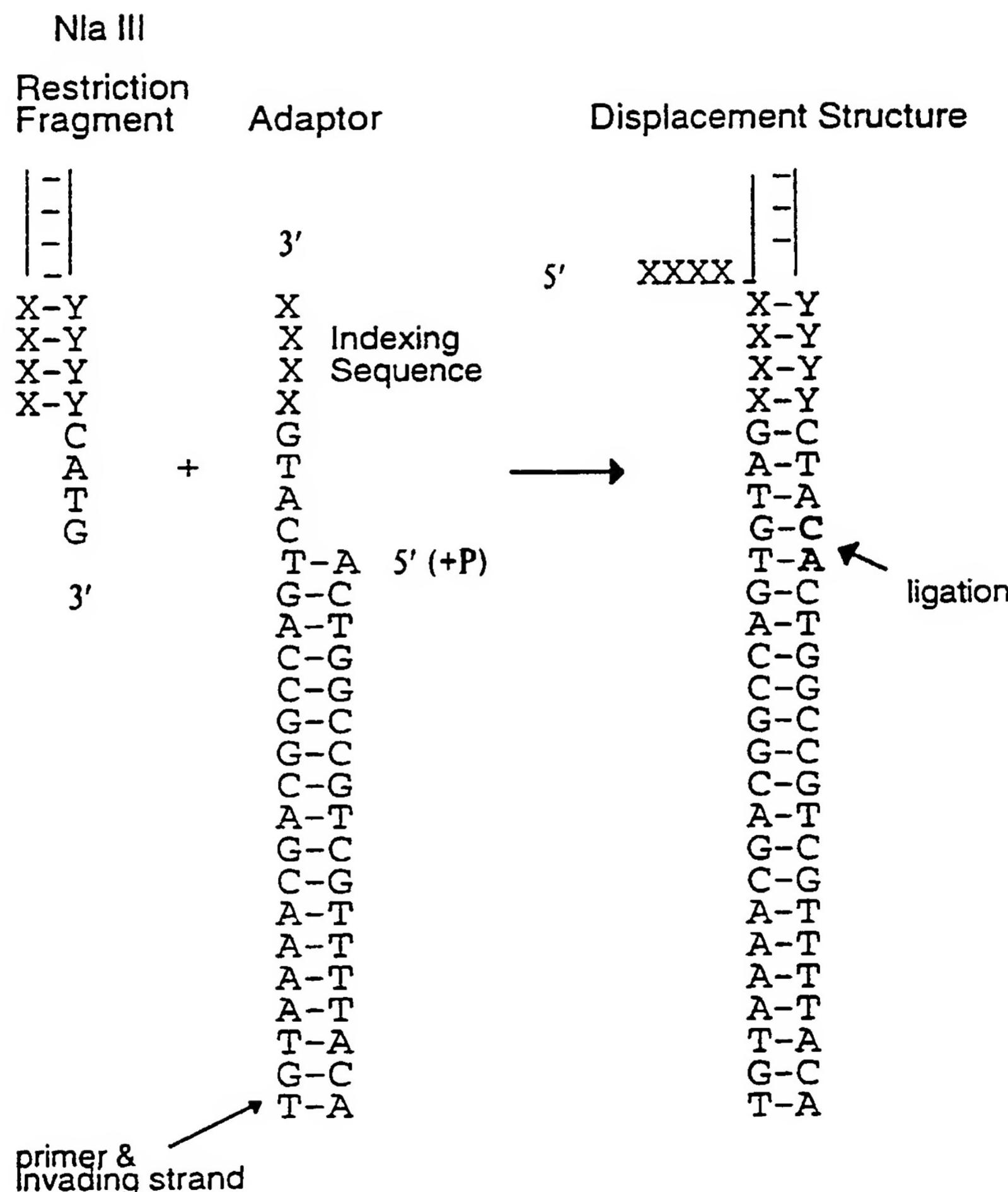


FIG. 3

PCR primer 1,2,3 sequencing primer 1,2,3

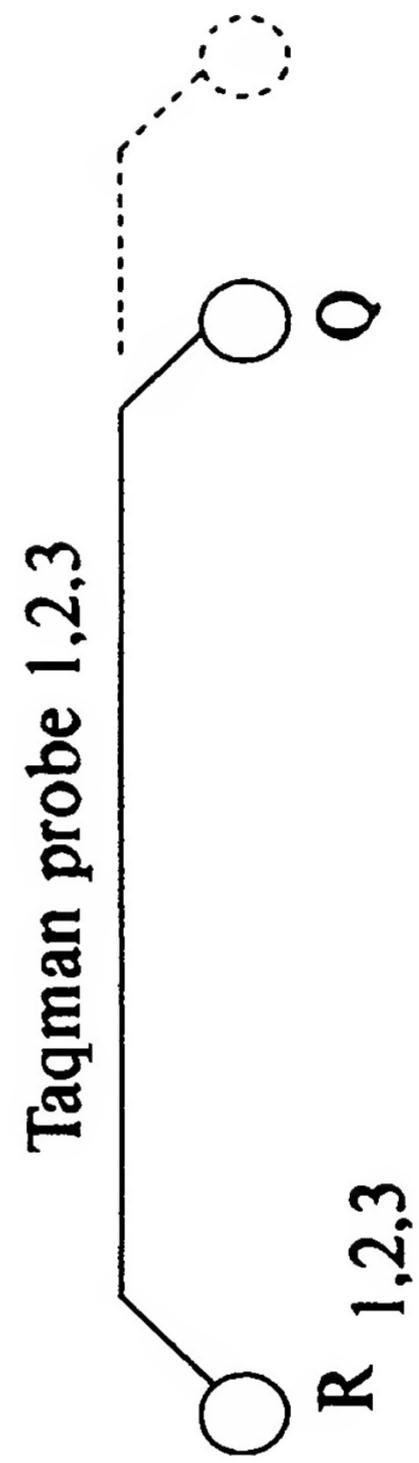
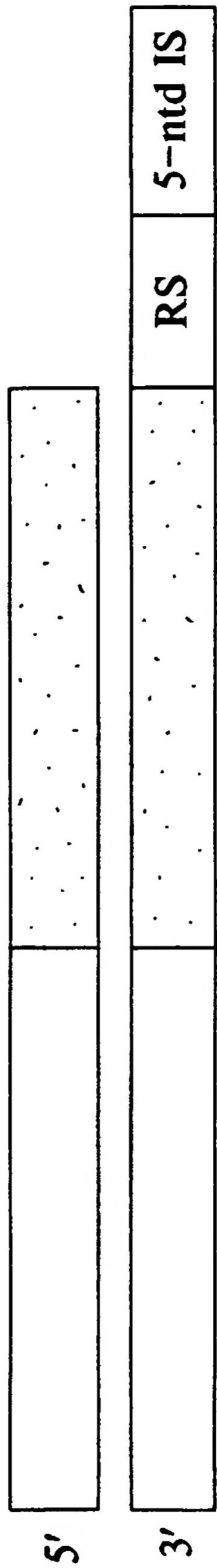
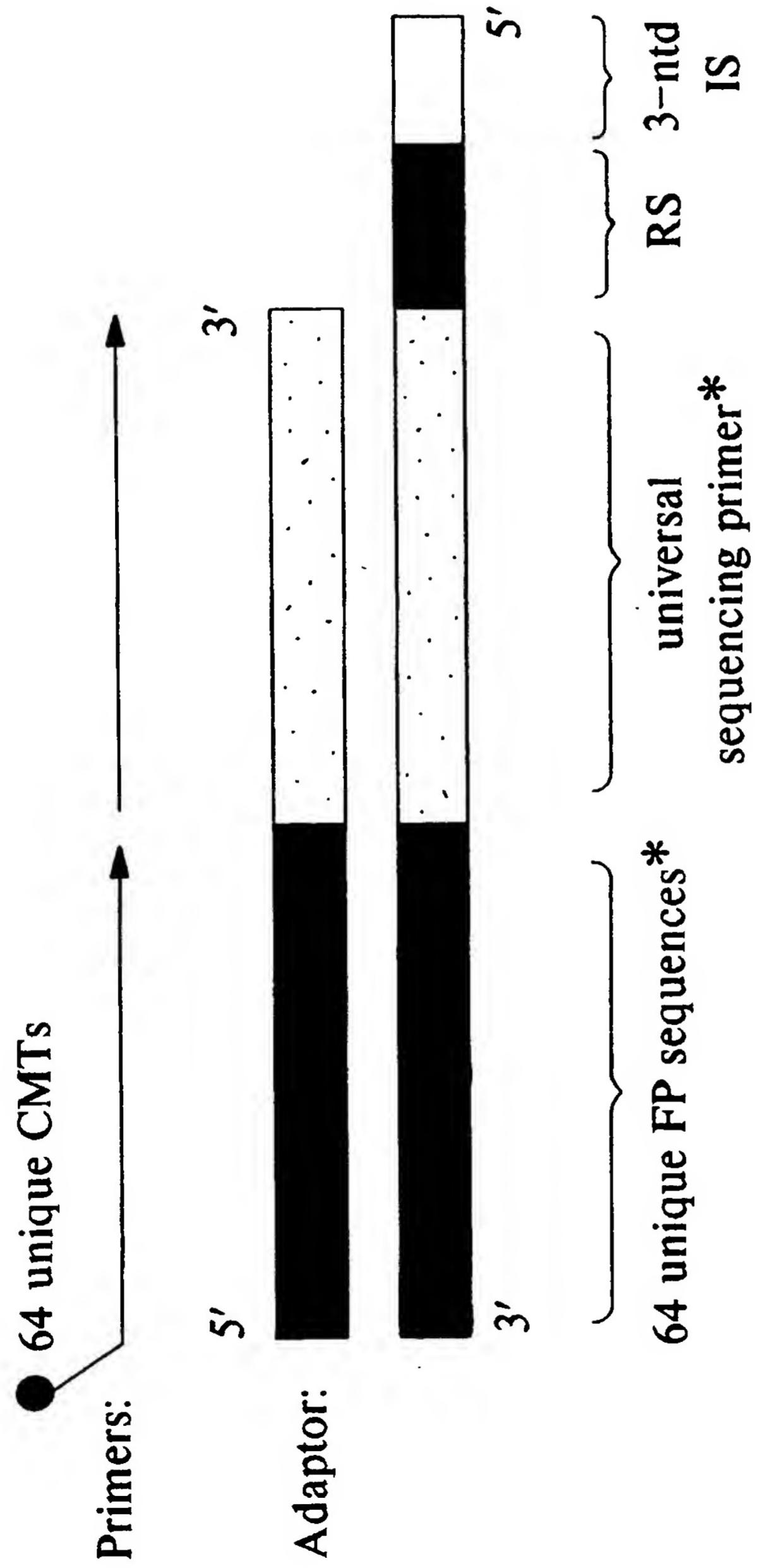


FIG. 4

5/5



FP = forward primer
RS = 4-cutter restriction site
IS = indexing sequence
CMT = cleavable mass tags

* can be 64 different sequencing primers

FIG. 5